



RAW SEQUENCE LISTING DATE: 04/21/2004
 PATENT APPLICATION: US/09/516,728A TIME: 08:01:00

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3 <110> APPLICANT: VANDERBILT UNIVERSITY
 4 DANIEL, THOMAS
 5 TAKAHASHI, TAKAMUNE
 6 MERNAUGH, RAYMOND
 8 <120> TITLE OF INVENTION: MODULATION OF ENDOTHELIAL CELL SURFACE RECEPTOR ACTIVITY IN THE
 9 REGULATION OF ANGIOGENESIS
 11 <130> FILE REFERENCE: 1242/12/2 CIP
 13 <140> CURRENT APPLICATION NUMBER: 09/516,728A
 14 <141> CURRENT FILING DATE: 2000-03-01
 16 <150> PRIOR APPLICATION NUMBER: US 09/152,160
 17 <151> PRIOR FILING DATE: 1998-09-10
 19 <160> NUMBER OF SEQ ID NOS: 4
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 8
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
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 34 <210> SEQ ID NO: 2
 35 <211> LENGTH: 4
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 39 <220> FEATURE:
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 44 Leu Ala Leu Ala
 45 1
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 54 <220> FEATURE:
 55 <221> NAME/KEY: CDS
 56 <222> LOCATION: (350)..(4363)
 58 <300> PUBLICATION INFORMATION:
 59 <301> AUTHORS: Ostman,A., Yang,Q. and Tonks,N.K.
 60 <302> TITLE: Expression of DEP-1, a receptor-like
 61 protein-tyrosine-phosphatase, is enhanced with increasing cell
 62 density
 63 <303> JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 64 <304> VOLUME: 91

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65 <305> ISSUE: 21
66 <306> PAGES: 9680-9684
67 <307> DATE: 1994-10-11
68 <308> DATABASE ACCESSION NO: U10886
69 <309> DATABASE ENTRY DATE: 1994-06-15
70 <313> RELEVANT RESIDUES: (1)..(5117)
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79 ctgccatgtc tccgggcaag ccggggcggg cggagcgggg acgaggcgga ccggctggcg      240
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83 ggcggggccc gattcgcgcg tccggggcac gttccagggc gcgcggggc atg aag ccg      358
84                                     Met Lys Pro
85                                     1
87 gcg gcg cgg gag gcg cgg ctg cct ccg cgc tcg ccc ggg ctg cgc tgg      406
88 Ala Ala Arg Glu Ala Arg Leu Pro Pro Arg Ser Pro Gly Leu Arg Trp
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92 Ala Leu Pro Leu Leu Leu Leu Leu Arg Leu Gly Gln Ile Leu Cys
93 20              25              30              35
95 gca ggt ggc acc cct agt cca att cct gac cct tca gta gca act gtt      502
96 Ala Gly Gly Thr Pro Ser Pro Ile Pro Asp Pro Ser Val Ala Thr Val
97      40              45              50
99 gcc aca ggg gaa aat ggc ata acg cag atc agc agt aca gca gaa tcc      550
100 Ala Thr Gly Glu Asn Gly Ile Thr Gln Ile Ser Ser Thr Ala Glu Ser
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103 ttt cat aaa cag aat gga act gga aca cct cag gtg gaa aca aac acc      598
104 Phe His Lys Gln Asn Gly Thr Gly Thr Pro Gln Val Glu Thr Asn Thr
105      70              75              80
107 agt gag gat ggt gaa agc tct gga gcc aac gat agt tta aga aca cct      646
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111 gaa caa gga tct aat ggg act gat ggg gca tct caa aaa act ccc agt      694
112 Glu Gln Gly Ser Asn Gly Thr Asp Gly Ala Ser Gln Lys Thr Pro Ser
113 100              105              110              115
115 agc act ggg ccc agt cct gtg ttt gac att aaa gct gtt tcc atc agt      742
116 Ser Thr Gly Pro Ser Pro Val Phe Asp Ile Lys Ala Val Ser Ile Ser
117      120              125              130
119 cca acc aat gtg atc tta act tgg aaa agt aat gac aca gct gct tct      790
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123 gag tac aag tat gta gta aag cat aag atg gaa aat gag aag aca att      838
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125      150              155              160
127 act gtt gtg cat caa cca tgg tgt aac atc aca ggc tta cgt cca gcg      886
128 Thr Val Val His Gln Pro Trp Cys Asn Ile Thr Gly Leu Arg Pro Ala
129      165              170              175
131 act tca tat gta ttc tcc atc act cca gga ata ggc aat gag act tgg      934

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136	Gly	Asp	Pro	Arg	Val	Ile	Lys	Val	Ile	Thr	Glu	Pro	Ile	Pro	Val	Ser	
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139	gat	ctc	cgt	gtt	gcc	ctc	acg	ggg	gtg	agg	aag	gct	gct	ctc	tcc	tgg	1030
140	Asp	Leu	Arg	Val	Ala	Leu	Thr	Gly	Val	Arg	Lys	Ala	Ala	Leu	Ser	Trp	
141				215						220					225		
143	agc	aat	ggc	aat	ggc	acc	gcc	tcc	tgc	cgg	gtt	ctt	ctt	gaa	agc	att	1078
144	Ser	Asn	Gly	Asn	Gly	Thr	Ala	Ser	Cys	Arg	Val	Leu	Leu	Glu	Ser	Ile	
145			230							235					240		
147	gga	agc	cat	gag	gag	ttg	act	caa	gac	tca	aga	ctt	cag	gtc	aat	atc	1126
148	Gly	Ser	His	Glu	Glu	Leu	Thr	Gln	Asp	Ser	Arg	Leu	Gln	Val	Asn	Ile	
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151	tcg	gac	ctg	aag	cca	ggg	gtt	caa	tac	aac	atc	aac	ccg	tat	ctt	cta	1174
152	Ser	Asp	Leu	Lys	Pro	Gly	Val	Gln	Tyr	Asn	Ile	Asn	Pro	Tyr	Leu	Leu	
153	260					265						270				275	
155	caa	tca	aat	aag	aca	aag	gga	gac	ccc	ttg	ggc	aca	gaa	ggg	ggc	ttg	1222
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159	gat	gcc	agc	aat	aca	gag	aga	agc	cgg	gca	ggg	agc	ccc	acc	gcc	cct	1270
160	Asp	Ala	Ser	Asn	Thr	Glu	Arg	Ser	Arg	Ala	Gly	Ser	Pro	Thr	Ala	Pro	
161				295						300					305		
163	gtg	cat	gat	gag	tcc	ctc	gtg	gga	cct	gtg	gac	cca	tcc	tcc	ggc	cag	1318
164	Val	His	Asp	Glu	Ser	Leu	Val	Gly	Pro	Val	Asp	Pro	Ser	Ser	Gly	Gln	
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167	cag	tcc	cga	gac	acg	gaa	gtc	ctg	ctt	gtc	ggg	tta	gag	cct	ggc	acc	1366
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172	Arg	Tyr	Asn	Ala	Thr	Val	Tyr	Ser	Gln	Ala	Ala	Asn	Gly	Thr	Glu	Gly	
173	340					345					350					355	
175	cag	ccc	cag	gcc	ata	gag	ttc	agg	aca	aat	gct	att	cag	gtt	ttt	gac	1462
176	Gln	Pro	Gln	Ala	Ile	Glu	Phe	Arg	Thr	Asn	Ala	Ile	Gln	Val	Phe	Asp	
177				360						365					370		
179	gtc	acc	gct	gtg	aac	atc	agt	gcc	aca	agc	ctg	acc	ctg	atc	tgg	aaa	1510
180	Val	Thr	Ala	Val	Asn	Ile	Ser	Ala	Thr	Ser	Leu	Thr	Leu	Ile	Trp	Lys	
181				375						380					385		
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184	Val	Ser	Asp	Asn	Glu	Ser	Ser	Ser	Asn	Tyr	Thr	Tyr	Lys	Ile	His	Val	
185			390							395					400		
187	gcg	ggg	gag	aca	gat	tct	tcc	aat	ctc	aac	gtc	agt	gag	cct	cgc	gct	1606
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189			405							410					415		
191	gtc	atc	ccc	gga	ctc	cgc	tcc	agc	acc	ttc	tac	aac	atc	aca	gtg	tgt	1654
192	Val	Ile	Pro	Gly	Leu	Arg	Ser	Ser	Thr	Phe	Tyr	Asn	Ile	Thr	Val	Cys	
193	420					425					430					435	
195	cct	gtc	cta	ggg	gac	atc	gag	ggc	acg	ccg	ggc	ttc	ctc	caa	gtg	cac	1702
196	Pro	Val	Leu	Gly	Asp	Ile	Glu	Gly	Thr	Pro	Gly	Phe	Leu	Gln	Val	His	

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203	acg gag atc ggc tta gca tgg agc agc cat gat gca gaa tca ttt cag						1798
204	Thr Glu Ile Gly Leu Ala Trp Ser Ser His Asp Ala Glu Ser Phe Gln						
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207	atg cat atc aca cag gag gga gct ggc aat tct cgg gta gaa ata acc						1846
208	Met His Ile Thr Gln Glu Gly Ala Gly Asn Ser Arg Val Glu Ile Thr						
209		485		490		495	
211	acc aac caa agt att atc att ggt ggc ttg ttc cct gga acc aag tat						1894
212	Thr Asn Gln Ser Ile Ile Ile Gly Gly Leu Phe Pro Gly Thr Lys Tyr						
213	500		505		510		515
215	tgc ttt gaa ata gtt cca aaa gga cca aat ggg act gaa ggg gca tct						1942
216	Cys Phe Glu Ile Val Pro Lys Gly Pro Asn Gly Thr Glu Gly Ala Ser						
217		520		525		530	
219	cgg aca gtt tgc aat aga act gtt ccc agt gca gtg ttt gac atc cac						1990
220	Arg Thr Val Cys Asn Arg Thr Val Pro Ser Ala Val Phe Asp Ile His						
221		535		540		545	
223	gtg gtc tac gtc acc acc acg gag atg tgg ctg gac tgg aag agc cct						2038
224	Val Val Tyr Val Thr Thr Thr Glu Met Trp Leu Asp Trp Lys Ser Pro						
225		550		555		560	
227	gac ggt gct tcc gag tat gtc tac cat tta gtc ata gag tcc aag cat						2086
228	Asp Gly Ala Ser Glu Tyr Val Tyr His Leu Val Ile Glu Ser Lys His						
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231	ggc tct aac cac aca agc acg tat gac aaa gcg att act ctc cag ggc						2134
232	Gly Ser Asn His Thr Ser Thr Tyr Asp Lys Ala Ile Thr Leu Gln Gly						
233	580		585		590		595
235	ctg att ccg ggc acc tta tat aac atc acc atc tct cca gaa gtg gac						2182
236	Leu Ile Pro Gly Thr Leu Tyr Asn Ile Thr Ile Ser Pro Glu Val Asp						
237		600		605		610	
239	cac gtc tgg ggg gac ccc aac tcc act gca cag tac aca cgg ccc agc						2230
240	His Val Trp Gly Asp Pro Asn Ser Thr Ala Gln Tyr Thr Arg Pro Ser						
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243	aat gtg tcc aac att gat gta agt acc aac acc aca gca gca act tta						2278
244	Asn Val Ser Asn Ile Asp Val Ser Thr Asn Thr Thr Ala Ala Thr Leu						
245		630		635		640	
247	agt tgg cag aac ttt gat gac gcc tct ccc acg tac tcc tac tgc ctt						2326
248	Ser Trp Gln Asn Phe Asp Asp Ala Ser Pro Thr Tyr Ser Tyr Cys Leu						
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251	ctt att gag aag gct gga aat tcc agc aac gca aca caa gta gtc acg						2374
252	Leu Ile Glu Lys Ala Gly Asn Ser Ser Asn Ala Thr Gln Val Val Thr						
253	660		665		670		675
255	gac att gga att act gac gct aca gtc act gaa tta ata cct ggc tca						2422
256	Asp Ile Gly Ile Thr Asp Ala Thr Val Thr Glu Leu Ile Pro Gly Ser						
257		680		685		690	
259	tca tac aca gtg gag atc ttt gca caa gta ggg gat ggg atc aag tca						2470
260	Ser Tyr Thr Val Glu Ile Phe Ala Gln Val Gly Asp Gly Ile Lys Ser						
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267	tcc	ttc	gac	tgc	gaa	gtg	gtc	ccc	aaa	gag	cca	gcc	ctg	gtt	ctc	aaa	2566
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269			725					730					735				
271	tgg	acc	tgc	cct	cct	ggc	gcc	aat	gca	ggc	ttt	gag	ctg	gag	gtc	agc	2614
272	Trp	Thr	Cys	Pro	Pro	Gly	Ala	Asn	Ala	Gly	Phe	Glu	Leu	Glu	Val	Ser	
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275	agt	gga	gcc	tgg	aac	aat	gcg	acc	cac	ctg	gag	agc	tgc	tcc	tct	gag	2662
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281				775						780					785		
283	tcg	tac	aac	atc	agc	atc	acc	act	gtg	tcc	tgt	gga	aag	atg	gca	gcc	2758
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288	Pro	Thr	Arg	Asn	Thr	Cys	Thr	Thr	Gly	Ile	Thr	Asp	Pro	Pro	Pro	Pro	
289			805						810				815				
291	gat	gga	tcc	cct	aat	att	aca	tct	gtc	agt	cac	aat	tca	gta	aag	gtc	2854
292	Asp	Gly	Ser	Pro	Asn	Ile	Thr	Ser	Val	Ser	His	Asn	Ser	Val	Lys	Val	
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295	aag	ttc	agt	gga	ttt	gaa	gcc	agc	cac	gga	ccc	atc	aaa	gcc	tat	gct	2902
296	Lys	Phe	Ser	Gly	Phe	Glu	Ala	Ser	His	Gly	Pro	Ile	Lys	Ala	Tyr	Ala	
297				840						845					850		
299	gtc	att	ctc	acc	acc	ggg	gaa	gct	ggg	cac	cct	tct	gca	gat	gtc	ctg	2950
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304	Lys	Tyr	Thr	Tyr	Asp	Asp	Phe	Lys	Lys	Gly	Ala	Ser	Asp	Thr	Tyr	Val	
305				870					875						880		
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312	Glu	Val	Leu	Lys	Tyr	Glu	Ile	Asp	Val	Gly	Asn	Glu	Ser	Thr	Thr	Leu	
313	900					905					910				915		
315	ggg	tat	tac	aat	ggg	aag	ctg	gaa	cct	ctg	ggc	tcc	tac	cgg	gct	tgt	3142
316	Gly	Tyr	Tyr	Asn	Gly	Lys	Leu	Glu	Pro	Leu	Gly	Ser	Tyr	Arg	Ala	Cys	
317				920						925					930		
319	gtg	gct	ggc	ttc	acc	aac	att	acc	ttc	cac	cct	caa	aac	aag	ggg	ctc	3190
320	Val	Ala	Gly	Phe	Thr	Asn	Ile	Thr	Phe	His	Pro	Gln	Asn	Lys	Gly	Leu	
321				935						940					945		
323	att	gat	ggg	gct	gag	agc	tat	gtg	tcc	ttc	agt	cgc	tac	tca	gat	gct	3238
324	Ile	Asp	Gly	Ala	Glu	Ser	Tyr	Val	Ser	Phe	Ser	Arg	Tyr	Ser	Asp	Ala	
325				950						955					960		
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valid <213> Response:

is of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

1#2

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